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SEQUENCE LISTING

<110> Gurney et al.

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<150> 60/155,493

<151> 1999-09-23

<150> 09/404,133

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65 70 75 80  
  
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95  
  
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110  
  
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125  
  
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140  
  
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160  
  
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175  
  
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190  
  
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro  
195 200 205  
  
Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220  
  
Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240  
  
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255  
  
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270  
  
Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285  
  
Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
 370 375 380

Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
 420 425 430

Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
 435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala  
450 455 460

Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp
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Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp  
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Ile Ser Leu Leu Lys  
500

<210> 9  
<211> 2088  
<212> DNA  
<213> *Homo sapiens*

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ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggaccaaa	180	
acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240	
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300	
ggccgcaagc	agtgcacagac	ccatccccac	tttgtgattc	cctaccgctg	cttagttggt	360	
gagtttgtaa	gtgatgccc	tctcggtcct	gacaagtgca	aatttttaca	ccaggagagg	420	
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aagagtacca	acttgcatg	ctacggcatg	ttgtcgccct	gcggaattgt	caagttccga	540	
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ccctacgaag	aagccacaga	gagaaccacc	agcattgcca	ccaccaccac	caccaccaca	840	
gagtctgtgg	aagaggtgg	tcgaggcct	acaacagcag	ccagtagcccc	tgatgccgtt	900	
gacaagtatc	tcgagacacc	tggggatgag	aatgaacatg	cccatttcca	gaaagccaaa	960	
gagaggctt	aggccaaqca	ccqagaaqqa	atqtccttca	tcatqaaqqa	atqqaqaaq	1020	

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ggttcaaaaca	aagggtgcaat	cattggactc	atgggtgggg	gtgtgtcat	agcgacagt	1920
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gtggaggttgc	acgcccgtgt	caccccaagag	gagcgccacc	tgtccaagat	gcagcagaac	2040
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<210> 10  
<211> 695  
<212> PRT  
<213> *Homo sapiens*

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 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45  
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 65 70 75 80  
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
 100 105 110  
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
 115 120 125  
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
 130 135 140  
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
 145 150 155 160  
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
 165 170 175  
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Val Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
 515 520 525  
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
 530 535 540  
 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
 545 550 555 560  
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
 565 570 575  
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
 580 585 590  
 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
 595 600 605  
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
 610 615 620  
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
 625 630 635 640  
 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
 645 650 655  
 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
 660 665 670  
 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
 675 680 685  
 Phe Phe Glu Gln Met Gln Asn  
 690 695

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<210> 11
<211> 2088
<212> DNA
<213> Homo sapiens
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacc 180
acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcaccq atgtggtaga agccaaccaa ccagtgcacca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatccccac ttgtgtattc cctaccgctg cttagttgt 360
gagttgtaa gtgatgccct ttcgttccct gacaagtgc aatttttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480
aagagtacca acttgcattt ctacggcatg ttgtgtccct gcggaaattga caagttccga 540
ggggtagagt ttgtgtttt cccactggct gaagaaaatg acaatgtgga ttctgtgtat 600
gcggaggagg atgactcgga tgtctgttgg ggccggacgc acacagacta tgcagatggg 660
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ccctacagaag aagccacaga gagaaccacc agcattgcac ccaccacca caccac 840
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gacaagatc tcgagacacc tggggatgg aatgaacatc cccatttcca gaaagccaaa 960
gagaggctt aggccaagca ccgagagaga atgtcccagg tcatgagaga atggaaagag 1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcatgtat ccagcattc 1080
caggagaaaag tggaaatctt ggaacaggaa gcagccaaacq aqagacacqca gctqqtggq 1140

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aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg 1320  
cgcatgggtt atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt 1380  
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gaggagattc aggatgaagt tcatgagctg cttagaaag agcaaaacta ttcaatgac 1500  
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tctttgaccc aaacgaaaac caccgtggag ctccttcccg tgaatggaga gttcagcctg 1620  
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atcgtcatca ccttgggtat gctgaagaag aaacagtaca catccattca tcatgggttg 1980  
gtggaggtt acgcccgtt caccggagag gagcgcacc ttttcaatgat gcagcagaac 2040  
ggctacgaaa atccaaaccta caagttttt gagcagatgc agaactag 2088

<210> 12

<211> 695

<212> PRT

<213> Homo sapiens

<400> 12

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

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<211> 2088  
<212> DNA  
<213> Homo sapiens

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tctttgaccg aaacgaaaac caccgtggag ctccttcccg tgaatggaga gttcagcctg 1620  
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ggctacgaaa atccaaccta caagttctt gagcagatgc agaactag 2088

<210> 14  
<211> 695  
<212> PRT  
<213> Homo sapiens

<400> 14  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

<210> 15

<211> 2094

<212> DNA

<213> Homo sapiens

<400> 15

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atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag 480  
aagagtacca acttgcattga ctacggcatg ttgtgccc gccaatttga caagttccga 540  
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gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
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gtggagggtt acgcccgtg caccggagag gagccacc tggccaagat gcagcagaac 2040  
ggctacgaaa atccaaccta caagttctt gagcagatgc agaacaagaa gtag 2094

<210> 16  
<211> 697  
<212> PRT  
<213> Homo sapiens

<400> 16  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
  
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

<210> 17

<211> 2094

<212> DNA

<213> Homo sapiens

<400> 17

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acctgcattt ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240  
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aagagtacca actgcatga ctacggcatg ttgtgcctt gcggaattga caagttccga 540  
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gaagccgatg atgacgagga cgatgaggat ggtgtatgagg tagaggaaga ggctgaggaa 780  
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atcgcatca cttgggtat gctgaagaag aaacagtaca catccattca tcatgggtg 1980  
gtggagggtt acggccgtt caccaggag gagccacc tttccaaatgat gcagcagaac 2040  
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<210> 18  
<211> 697  
<212> PRT  
<213> Homo sapiens

<400> 18  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255  
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Val Ile Ala Thr Val  
625 630 635 . 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

<210> 19  
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<212> DNA  
<213> *Homo sapiens*

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<212> PRT  
<213> Homo sapiens

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255  
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270  
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Val Ile Ala Thr Val  
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 . . . 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

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<210> 21
<211> 1341
<212> DNA
<213> Homo sapiens
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	aggggcaga	cggggcaggg	ctactacgt	gagatgaccg	tgggcagccc	cccgcagacg	240
	ctcaacatcc	tggtgat	aggcagcagt	aactttgcag	tggtgtctgc	cccccacccc	300
	ttcctgcac	gctactacca	gaggcagctg	tccagcacat	accgggacct	ccggaagggt	360
	gtgtatgtc	cctacaccca	ggcaagtgg	gaaggggagc	tgggcaccga	cctgttaagc	420
	atccccatg	gccccaaacgt	cactgtgcgt	gccaacatg	ctgcacatcac	tgaatcagac	480
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	cgggccc	aacgaattgg	ctttgtgtc	agcgcttgc	atgtgcacga	tgagttcagg	1260
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<210> 22  
<211> 446  
<212> PRT  
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<400> 22

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Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser  
50 55 60

Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr  
65 70 75 80

Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala  
85 90 95

Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser  
100 105 110

Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly  
115 120 125

Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly  
130 135 140

Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp  
145 150 155 160

Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala  
165 170 175

Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp  
180 185 190

Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu  
195 200 205

Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val  
210 215 220

Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly  
225 230 235 240

Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile  
245 250 255

Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys  
260 265 270

Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu  
275 280 285

Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala  
290 295 300

Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln  
305 310 315 320

Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val  
325 330 335

Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile  
340 345 350

Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr  
355 360 365

Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly  
370 375 380

Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp  
385 390 395 400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His  
405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp  
420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
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<210> 23

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 23

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ggccggaggg gcagcttgc ggagatggtg gacaacctga ggggcaagtc ggggcaggggc 240  
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gagcctttct ttgactctct ggtaaaggcag acccacgttc ccaacctctt ctccctgcac 660  
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<210> 24

<211> 459

<212> PRT

<213> Homo sapiens

<400> 24

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Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg  
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Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly  
50 55 60

Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly  
65 70 75 80

Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile  
85 90 95

Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His  
100 105 110

Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg  
115 120 125

Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu  
130 135 140

Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val  
145 150 155 160

Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe  
165 170 175

Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu  
180 185 190

Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val  
195 200 205

Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala  
210 215 220

Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser  
225 230 235 240

Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp  
245 250 255

Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg  
260 265 270

Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn  
275 280 285

Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro  
290 295 300

Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser  
305 310 315 320

Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys  
325 330 335

Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu  
340 345 350

Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu  
355 360 365

Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp  
370 375 380

Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met  
385 390 395 400

Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg  
405 410 415

Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe  
420 425 430

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp  
435 440 445

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
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<210> 25

<211> 1302

<212> DNA

<213> Homo sapiens

<400> 25

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<210> 26

<211> 433

<212> PRT

<213> Homo sapiens

<400> 26

Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly  
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Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu  
20 25 30

Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg  
35 40 45

Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro  
50 55 60

Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala  
65 70 75 80

Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln  
85 90 95

Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr  
100 105 110

Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile  
115 120 125

Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr  
130 135 140

Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu  
145 150 155 160

Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro  
165 170 175

Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser  
180 185 190

Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu  
195 200 205

Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu  
210 215 220

Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr  
225 230 235 240

Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met  
245 250 255

Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr  
260 265 270

Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser  
275 280 285

Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu  
290 295 300

Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile  
305 310 315 320

Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser  
325 330 335

Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp  
340 345 350

Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser  
355 360 365

Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val  
370 375 380

Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys  
385 390 395 400

His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val  
405 410 415

Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu  
420 425 430

Ser

<210> 27  
<211> 1278

<212> DNA

<213> Homo sapiens

<400> 27

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<210> 28

<211> 425

<212> PRT

<213> Homo sapiens

<400> 28

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Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe  
20 25 30

Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr  
35 40 45

Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val  
50 55 60

Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe  
65 70 75 80

Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu  
85 90 95

Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu  
100 105 110

Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val  
115 120 125

Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn  
130 135 140

Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala  
145 150 155 160

Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln  
165 170 175

Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe  
180 185 190

Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile  
195 200 205

Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr  
210 215 220

Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu  
225 230 235 240

Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp  
245 250 255

Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys  
260 265 270

Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu  
275 280 285

Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln  
290 295 300

Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu  
305 310 315 320

Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln  
325 330 335

Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys  
340 345 350

Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala  
355 360 365

Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg  
370 375 380

Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr  
385 390 395 400

Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly  
405 410 415

Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
420 425

<210> 29  
<211> 1362  
<212> DNA  
<213> Homo sapiens

<400> 29

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catgtgcacg atgagttcag gacggcagcg gtggaaaggcc ctttgcac ctggacatg 1320  
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<210> 30

<211> 453

<212> PRT

<213> Homo sapiens

<400> 30

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser  
450

<210> 31  
<211> 1380  
<212> DNA

<213> Homo sapiens

<400> 31

atggcccaag ccctgccctg gtcctgctg tggatggcg cggagtgct gcctgcccac 60  
ggcacccagc acggcatccg gctgccctg cgacgcccgc tggggggcgc ccccctgggg 120  
ctggcgctgc cccggagac cgacgaagag cccgaggagc cggccggag gggcagctt 180  
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtggcagcc ccccgagac gctcaacatc ctggtgata caggcagcag taactttgca 300  
gtgggtgctg ccccccaccc cttccctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccgaaaggg tggatgtg ccctacaccc agggcaagt ggaaggggag 420  
ctgggcaccc acctgtaag catccccat gcccccaacg tcactgtcg tgccaacatt 480  
gctgccatca ctgaatcaga caagttctc atcaacggct ccaactggga aggcacccctg 540  
ggctggcct atgctgagat tgccaggct gacgactccc tggagccctt cttgactct 600  
ctggtaaagc agaccacgt tcccaaccc tcctccctgc acctttgtgg tgctggctc 660  
ccctcaacc agtctgaagt gctggcctt gtcggaggga gcatgatcat tggaggtatc 720  
gaccactcgc tgcacacagg cagtctctgg tatacacca tccggggga gtggattat 780  
gaggtcatca ttgtcggtt ggagatcaat ggacaggatc tgaaaatggg ctgcaaggag 840  
tacaactatg acaagagcat tggatggcactt ggcacccacca accttcgttt gccaagaaaa 900  
gttttgaag ctgcgtcaa atccatcaag gcagccctc ccacggagaa gttccctgtat 960  
gtttctggc taggagagca gctgggtgtc tggcaaggag gcaccacccc ttggAACATT 1020  
ttccctggc tctcactcta ctaatgggt gaggtacca accagtcctt ccgcaccc 1080  
atccctccgc agcaataacct gcccggcagt gaaatgtgg ccacgtccca agacgactgt 1140  
tacaagttt ccacatcaca gtcatccacg ggcactgtt tggagctgt tatcatggag 1200  
ggcttctacg ttgtcttga tccggcccgaa aacgaaattt gctttgtgt cagcgcttgc 1260  
catgtgcacg atgagttcag gacggcagcg gtggaaaggcc ctttgcac ctggacatg 1320  
gaagactgtg gctacaacat tccacagaca gatgagtcac agcagcagca gcagcagtga 1380

<210> 32

<211> 459

<212> PRT

<213> Homo sapiens

<400> 32

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser His His His His His His His  
450 455

<210> 33

<211> 25

<212> PRT  
<213> Homo sapiens

<400> 33  
Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu  
1 5 10 15  
Ser Ser Leu Val Arg His Arg Trp Lys  
20 25

<210> 34  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 34  
Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser  
1 5 10 15  
Leu Leu Lys

<210> 35  
<211> 29  
<212> DNA  
<213> Homo sapiens

<400> 35  
gtggatccac ccagcacggc atccggctg

29

<210> 36  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 36  
gaaagcttc atgactcatc tgtctgtgga atgttg

36

<210> 37  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 37  
gatcgatgac tatctctgac tctccgcgtg aacaggacg

39

<210> 38  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 38  
gatccgtcct gttcacgcgg agagtcagag atagtcatc

39

<210> 39  
<211> 77  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2

<400> 39  
cgccatccgg ctgcccctgc gtagcggtct gggtggtgct ccactgggtc tgcgtctgcc 60  
ccgggagacc gacgaag 77

<210> 40  
<211> 77  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2

<400> 40  
cttcgtcggt ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60  
ggggcagccg gatgccg 77

<210> 41  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 41  
gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 42  
gatccgtcgg tttcgataacc agagtccagc ggagagtcag agatagtcat c 51

<210> 43  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 43  
aaggatcct tgtggagatg gtggacaacc tg 32

<210> 44  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 44  
gaaagcttc atgactcatc tgtctgtgga atgttg 36

<210> 45  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 6-His tag

<400> 45  
gatcgcatca tcaccatcac catg 24

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 6-His tag

<400> 46  
gatccatggt gatggtagt atgc 24

<210> 47  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 47  
gactgaccac tcgaccaggt tc 22

<210> 48  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 48  
cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51

<210> 49  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 49  
cgaattaaat tccagcacac tggcta 26

<210> 50  
<211> 1287  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2(b)  
delta TM

<400> 50  
atggcccaag ccctgccctg gctcctgctg tggatggcg cgggagtgct gcctgcccac 60  
ggcacccagc acggcatccg gctgccccctg cgacgccccg tggggggcgc cccccctgggg 120  
ctgcggctgc cccgggagac cgacgaagag cccgaggagc cccggccggag gggcagctt 180  
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtggcagcc ccccgccagac gctcaacatc ctggtgata caggcagcag taactttgca 300  
gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360

taccgggacc tccggaaggg tggatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccc acctggtaag catccccat ggccccaacg tcactgtgcg tgccaacatt 480  
gctgccatca ctgaatcaga caagttctc atcaacggct ccaactggga aggcattctg 540  
ggctggccat atgctgagat tgccaggctt tgggtgctg gcttccccct caaccagtct 600  
gaagtgtgg cctctgtcg aggagcatg atcattggag gtatcgacca ctcgctgtac 660  
acaggcagtc tctgtatac acccatccgg cgggagtggt attatgaggt catcattgtg 720  
cgggtggaga tcaatggaca ggtctgaaa atggactgca aggagtacaa ctatgacaa 780  
agcattgtgg acagtggcac caccacccct cgttggccca agaaagtgtt tgaagctgca 840  
gtcaaatcca tcaaggcagc ctcctccacg gagaagttcc ctgatgttt ctggcttagga 900  
gagcagctgg tggctggca agcaggcacc accccttggaa acattttccc agtcatctca 960  
ctctacctaa tgggtgaggt taccacccag tccttccgca tcaccatcct tccgcagcaa 1020  
tacctgcggc cagtggaaga tggccacg tcccaagacg actgttacaa gttgcccattc 1080  
tcacagtcat ccacgggcac tggatggaa gctgttatca tggagggctt ctacgttgac 1140  
tttgatcgaa cccgaaaacg aattggctt gctgtcagcg cttgcccattgt gcacgatgag 1200  
ttcaggacgg cagcgttgg aggcccttt gtcacccatgg acatggaaaga ctgtggctac 1260  
aacattccac agacagatga gtcatga 1287

<210> 51  
<211> 428  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2(b)  
delta TM

<400> 51  
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15  
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30  
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45  
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60  
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80  
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95  
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110  
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125  
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140  
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160  
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175  
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly  
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser  
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile  
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
420 425

<210> 52  
<211> 1305  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2(b)  
delta TM

<400> 52  
atggcccaag ccctgccctg gtcctgctg tggatggcg cggagtgct gcctgcccac 60  
ggcacccagc acggcatccg gctgccctg cgcacggcc tggggggcgc ccccctgggg 120  
ctgcggctgc cccggagac cgacqaagag cccqaggagc cggccggag gggcagctt 180  
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtgggcagcc ccccgagac gctcaacatc ctggtgata cagggcagcag taactttgca 300  
gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg ttgttatgtg ccctacaccc agggcaagtg ggaaggggag 420

ctgggcaccc acctggtaag catccccat ggccccaacg tcactgtgcg tgccaacatt 480  
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattctg 540  
gggctggcct atgctgagat tgccaggcgt tggctgtcg gcttccccct caaccagtct 600  
gaagtgtgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660  
acaggcagtc tctggatac acccatccgg cgggagtggt attatgaggt catcattgtg 720  
cgggtggaga tcaatggaca gatatctgaaa atggactgca aggagtacaa ctatgacaag 780  
acattgtgg acatgggcac caccaacctt cgttgccc agaaagtgtt tgaagctgca 840  
gtcaaatcca tcaaggcagc ctcctccacg gagaagttcc ctgatggtt ctggcttagga 900  
gagcagctgg tggctggca agcaggcacc accccttggaa acatttccc agtcatctca 960  
ctctacctaa tgggtgaggt taccacccag tccttccgca tcaccatcct tccgcagcaa 1020  
tacctgcggc cagtggaaga tggccacg tcccaagacg actgttacaa gttgccatc 1080  
tcacagtcat ccacgggcac tggatggga gctgttatca tggagggctt ctacgttgc 1140  
tttgatcggg cccgaaaacg aattggctt gctgtcagcg cttgccatgt gcacgatgag 1200  
ttcaggacgg cagcgttggaa aggcccttt gtcaccttgg acatggaga ctgtggctac 1260  
aacattccac agacagatga gtcacagcag cagcagcagc agtga 1305

<210> 53

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)  
delta TM

<400> 53

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly  
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser  
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile  
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His  
420 425 430

His His

<210> 54  
<211> 2310  
<212> DNA  
<213> Homo sapiens

<400> 54  
atgctgcccc gttggcaact gtcctgctg gccgcctgga cggctcgccc gctggaggta 60  
cccaactgatg gtaatgctgg cctgctggct gaacccaga ttgccatgtt ctgtggcaga 120  
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
acctgcattg ataccaagga aggcacatctg cagtattgcc aagaagtcta ccctgaactg 240  
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaaggc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttgg 360

gagtttgtaa gtgatgccct ttcgttccct gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaactca tttcaactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtacca acttgcatga ctacggcatg ttgtgtccct gcggattga caagttccga 540  
gggttagagt ttgtgtttt cccactggct gaagaaagtg acaatgtggat ttctgtgtat 600  
gcggaggagg atgactcgga tttctgtgg ggcggagcg acacagacta tgcatgtgg 660  
agtgaagaca aagtagtaga agtagcagag gaggagaag tggctgaggt ggaagaagaa 720  
gaagccgatg atgacgagga cgatgaggat ggtgtatggg tagaggaaga ggctgaggaa 780  
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840  
gagtctgtgg aagaggtgg tcgagagggt tgctctgaac aagccgagac gggccgtgc 900  
cgagcaatga tctcccgctg gtactttgtat gtgactgaag ggaagtgtgc cccattctt 960  
tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg 1020  
tgtggcagcg ccatgtccca aagtttactc aagactaccc aggaacctct tgccgagat 1080  
cctgttaaac ttcctacaac agcagccagt acccctgtat ccgttgacaa gtatctcgag 1140  
acacctgggg atgagaatga acatgcccatttccagaaag ccaaagagag gcttgaggcc 1200  
aagcaccgag agagaatgtc ccaggtcatg agagaatggg aagaggcaga acgtcaagca 1260  
aagaacttgc ctaaagctga taagaaggca gttatccagc atttccagga gaaagtggaa 1320  
tcttggaaac aggaagcagc caacgagaga cagcagctgg tggagacaca catggccaga 1380  
gttggaaacca tgctcaatga ccggccggcc ctggccctgg agaactacat caccgctctg 1440  
caggctgttc ctctccggcc tctgtcacgtt tcataatgc taaagaagta tttccggcga 1500  
gaacacaagg acagacagca caccctaaag catttcgagc atgtgcgcatttggatccc 1560  
aagaaaagccg ctcatccg gttcccgaggat atgacacacc tccgtgtat ttatgagcgc 1620  
atgaatcagt ctctccctt gctctacaac gtgcctgcag tggccgagga gattcaggat 1680  
gaagttgatg agctgcttca gaaagagcaa aactattcag atgacgtctt ggcacacatg 1740  
attagtgaac caaggatcag ttacggaaac gatgcctca tgccatctt gaccgaaacg 1800  
aaaaccaccc tggagcttcc tccctgtat ggagagttca gcctggacga tctccagccg 1860  
tggcattctt ttggggctga ctctgtgcca gccaacacag aaaacgaagt tgagcctgtt 1920  
gatgcccggcc ctgctccga ccgaggactg accactcgac caggttctgg gttgacaaat 1980  
atcaagacgg aggagatctc tgaagtgaag atggatgcag aattccgaca tgactcagga 2040  
tatgaagttc atcatcaaaa attgggtttc ttttcgagaag atgtgggttc aaacaaaggt 2100  
gcaatcattt gactcatggt gggcggtgtt gtcatagcg cagtgatcgt catcaccttg 2160  
gtgatgctga agaagaaaca gtacacatcc attcatcatg gtgtgggtga gtttgcgc 2220  
gctgtcaccctt cagaggagcg ccacctgtcc aagatgcagc agaacggcta cgaaaatcca 2280  
acctacaagt tctttgagca gatgcagaac 2310

<210> 55

<211> 770

<212> PRT

<213> Homo sapiens

<400> 55

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Ala Val Ile  
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn  
770

<210> 56  
<211> 2253  
<212> DNA  
<213> Homo sapiens

<400> 56

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacaaa 180  
acctgcattt ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240  
cagatcacca atgtgttaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtcaagac ccattccccac tttgtgattt cctaccgctg cttagttgg 360  
gagtttgtaa gtgatgccct tctcgccct gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtacca acttgcattga ctacggcatg ttgtgcctt gcggaattga caagttccga 540  
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gagtctgtgg aagagggtgg tgcagaggtt tgctctgaac aagccgagac gggggcgtgc 900  
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gagacacctg gggatgagaa tgaacatgcc catttccaga aagccaaaga gaggcttgag 1140  
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gcagaacaga aggacagaca gcacaccata aagcatttgc agcatgtgcg catgggtggat 1500  
cccaaggaaag ccgctccatg ccgggtcccaag gttatgacac acctccgtgt gatttatgag 1560  
cgcattgtatc agtctctctc cctgtcttac aacgtgcctg cagtgccatc tgactctgtg 1620  
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ccgtggcatt cttttggggc tgactctgtg ccagccaaca cagaaaacga agttgagctt 1860  
gttgatgccc gccctgtgc cgaccggagg ctgaccactc gaccagggttc tgggttgaca 1920  
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ggatatgaag ttcatcatca aaaattgggtt ttctttgcag aagatgtggg ttcaaacaaa 2040  
ggtgcaatca ttggactcat ggtggggcgtt gttgtcatag cgacagtgtat cgtcatcacc 2100  
ttgggtgatgc tgaagaagaa acagtacaca tccattcatc atgggtgtggt ggaggttgac 2160  
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ccaaacctaca agttcttgcg cagatgcac aac 2253

<210> 57  
<211> 751  
<212> PRT  
<213> Homo sapiens

<400> 57

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr  
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu  
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg  
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln  
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe  
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln  
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp  
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val  
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg  
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val  
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met  
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu  
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp  
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn  
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro  
565 570 575

Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly  
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp  
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg  
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr  
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe  
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe  
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val  
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu  
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp  
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn  
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn  
 740 745 750

<210> 58  
<211> 2316  
<212> DNA  
<213> *Homo sapiens*

<210> 59  
<211> 772  
<212> PRT  
<213> *Homo sapiens*

<400> 59  
Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
                  20                 25                         30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn Lys Lys  
770

<210> 60  
<211> 2259  
<212> DNA  
<213> Homo sapiens

<400> 60  
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180  
acctgcattt ataccaagga aggcatctg cagtattgcc aagaagtcta ccctgaactg 240  
cagatcacca atgtggtaga agccaacccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtgcacagac ccatccccac tttgtgattt cctaccgtt ctttagttgg 360  
gagtttggtaa gtgatgccc ttcgttccct gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagttacca acttgcatga ctacggcatg ttgctgccc gcggaattga caagttccga 540  
ggggtagatgt ttgtgtgtt cccactggct gaagaaagtgc acaatgttgc ttctgtgtat 600  
gcccggaggat atgactcgga tgcgttggc ggcggggcgc acacagacta tgcagatggg 660  
agtgaagaca aagttagtgc aagtgcacgc gaggaaaga 720  
gaagccgatg atgacggaggat cgtggatgtt ggtgtatggc tagggaaa ggtggaggaa 780  
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cgagcaatga tctcccgctg gtactttgtat gtgactgaag ggaagtgtgc cccattcttt 960  
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gagacacctg gggatggaaa tgaacatgcc catttccaga aagccaaaga gaggcttgag 1140  
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gcaaagaact tgcctaaagc tgataagaag gcagttatcc agcatttcca ggagaaagtgc 1260  
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agagtggaaat ccatgctcaa tgaccggccgc cgccctggccc tggagaacta catcaccgc 1380  
ctgcaggctg ttccctctcg gcctcgatc gtgttcaata tgctaaagaa gtatgtccgc 1440  
gcagaacaga aggacagaca gcacacccta aagcatttcg agcatgtgcg catggtgat 1500  
cccaagaaat ccgtcgat ccgggtcccg gttatgacac acctccgtgt gatttatgag 1560  
cgcatgaatc agtctctctc cctgtcttac aacgtgcctg cagtggccga ggagattcag 1620  
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acgaaaacca ccgtggatgt cttttccgtg aatggggatgt tcagccttggc cgtatctcccg 1800  
ccgtggatgt cttttgggc tgactctgt ccagccaaaca cagaaaacga agttgagcc 1860  
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ttgggtatgatc tgaagaagaa acgtacaca tccattcatc atgggttgatggagttgac 2160  
gccgctgtca ccccaagagga gcccacccctg tccaaagatgc agcagaacgg ctacgaaaat 2220  
ccaaacccatca agttcttgc gcaatgcac aacaagaag 2259

<210> 61  
<211> 753  
<212> PRT  
<213> Homo sapiens

<400> 61  
Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
1 5 10 15  
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30  
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255  
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270  
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285  
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr  
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu  
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg  
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln  
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe  
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln  
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp  
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val  
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg  
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val  
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met  
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu  
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp  
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn  
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro  
565 570 575

Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly  
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp  
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg  
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr  
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe  
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe  
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val  
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu  
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp  
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn  
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys  
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Lys

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